

CLAIMS

1/ A method for the production of a complex cDNA mixture by reverse transcription of mRNA from tissues or cells, characterized by the addition, in the mRNA reaction mixture, of elongation terminators, recovery of the cDNA mixture formed, preferably followed by its purification.

2/ A method according to Claim 1, characterized by the use of dideoxynucleotides as elongation terminators.

3/ Kits for the synthesis of cDNA mixtures according to the method of Claim 1 or 2, characterized in that they contain, in addition, reagents for carrying out reverse transcription, elongation terminators, especially dideoxynucleotides, and instructions for use.

4/ cDNA mixtures as obtained by implementation of the method according to Claim 1 or 2, reliably reflecting the state of transcription of a tissue or of cells, i.e. the number and the level of gene expression.

5/ The use of complex cDNA mixtures according to Claim 4, as hybridization probes.

6/ A method for investigating gene expression profiles in a tissue or in cells, characterized in that it comprises bringing cDNA mixtures according to Claim 4 into contact with the DNA to be studied (cDNA, or specific oligonucleotides or DNAs), in conditions permitting the hybridization of complementary sequences when they are present.

7/ Application of the method according to one of the Claims 1 or 2 in cDNA production by reverse transcription starting from mRNA's from a tissue or from a cell,

Replaced by Article 34

especially with the aim of determining the level of gene expression by counting cloned and sequenced cDNA's, for example by the SAGE method or partial sequencing of cDNA libraries.